

FIGURE 1

HSP 90-beta (Mouse)

SEQ ID NO:1

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1 mpeevhhgee evetfafqae iaqlmsliin tfysnkeifl relisnasda ldkiryeslt
61 dpskldsgke lkidiipnpq ertltlvdtg igmtkadlin nlgtiaksgt kafmealqag
121 adismigqfg vgfysaylva ekvvvitkhn ddegyawess aggsftvrad hgepigrgtk
181 vilhlkedqt eyleerrvke vvkkhsqfig ypitlyleke rekeisdeea eeekgeeee
241 dkdddeekpki edvgsdeedd sgdkkkktk kikekyidqe elnktpiwt rnpdditqee
301 ygefyksltm dwedhlavkh fsveggolefr allfiprrap fd1fenkkkk nniklyvrrv
361 fimdscdeli peylnfirgv vdsedlplni sremlqqski lkvirknivk kcelfsel
421 edkenykkfy eafsknlklg ihedstnrrr lsellryhts qsgdemtsls eyvsrmketq
481 ksiiyyitges keqvansafv ervrkrgfev vymtepidey cvqqlkefdg kslvsvtkeg
541 lelpdedeeek kkmeeskakf enlcklmkei ldkkvekvti snrlvsspcc ivtstygwta
601 nmerimkaqa lrdnstmgym makkhleinp dhpivetlrq kaeakndka vndlvvllfe
661 tallssgfsl edpqthsnri yrmiklgli dedevaeeep naavpdeipp legdedasrm
721 eevd

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HSP 90-beta (Human)

SEQ ID NO:2

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1 mpeevhhgee evetfafqae iaqlmsliin tfysnkeifl relisnasda ldkiryeslt
61 dpskldsgke lkidiipnpq ertltlvdtg igmtkadlin nlgtiaksgt kafmealqag
121 adismigqfg vgfysaylva ekvvvitkhn ddegyawess aggsftvrad hgepigrgtk
181 vilhlkedqt eyleerrvke vvkkhsqfig ypitlyleke rekeisdeea eeekgeeee
241 dkdddeekpki edvgsdeedd sgdkkkktk kikekyidqe elnktpiwt rnpdditqee
301 ygefyksltm dwedhlavkh fsveggolefr allfiprrap fd1fenkkkk nniklyvrrv
361 fimdscdeli peylnfirgv vdsedlplni sremlqqski lkvirknivk kcelfsel
421 edkenykkfy eafsknlklg ihedstnrrr lsellryhts qsgdemtsls eyvsrmketq
481 ksiiyyitges keqvansafv ervrkrgfev vymtepidey cvqqlkefdg kslvsvtkeg
541 lelpdedeeek kkmeeskakf enlcklmkei ldkkvekvti snrlvsspcc ivtstygwta
601 nmerimkaqa lrdnstmgym makkhleinp dhpivetlrq kaeakndka vndlvvllfe
661 tallssgfsl edpqthsnri yrmiklgli dedevaeeep naavpdeipp legdedasrm
721 eevd

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HSP 90-alpha (Human)

SEQ ID NO:3

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1 mpeetqtqdq pmeeeevetf afqaeiaqlm sliintfysn keiflrelis nssdaldkir
61 yesltdpskl dsgkelhnl ipnkqdrtlt ivdtgigmtk adlinnlgti aksgtkafme
121 alqagadism igqfvvgfys aylvaektv itkhnddegy awessaggf tvrttgtpepm
181 grgtkvilhl kedqteylee rrikeivkh sqfigypitl fvekerdkev sddeaeeked
241 keekekeek esedkpeied vgsdeeeeek dgdkkkkkki kekyidqeel nktkpiwtrn
301 pdeditneeyg efykstndw edhlavkhfs vegglefral lfvprrapfd lfenrkknn
361 iklyvrrvfi mdnceelipe ylnfirgvvd sedlplnisi emlqqskilk virknlvkcc
421 lelf telaed kenykkfyeq fskniklgih edsqrkkls ellryytsas gdemvslkdy
481 ctrmkengkh iyyitgetkd qvansafver lrkhgleviy miepideycv qqlkefegkt
541 lvsutkegle lpedeekkk geekktkfen lckimkdile kkvekvvvsn rlvtspcciv
601 tstygtamm erimkaqa lrdnstmgymaa khleinpdh sietlrqka eadkndksvk
661 dlvillyeta llssgfsl edpqthsnri yrmiklgli dedevaeeep naavpdeipp avteempple
721 gdddttsrmee vd

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HSP 84 (Mouse)
SEQ ID NO:4

1 mpeevhhgee evetfafqae iaqlmsliin tfysnkeifl relisnasda ldkiryeslt
 61 dpskldsgke lkidiipnpq ertltlvdtg igmtkadlin nlgtiaksgt kafmealqag
 121 adismigqfg vgfysaylva ekvvvitkhn ddegyawess aggsftvrad hgepigrgtk
 181 vilhikedqt eyleerrvke vvkkhsqfig ypitlyleke rekeisddea eeekgekeee
 241 dkdedeekpki edvgsdeedd sgdkkkktk kikekyidqe elnktpiwt rnpdditqee
 301 ygefyksltn dwedhlavkh fsveggolefr allfiprrap fdlfenkkkk nniklyvrrv
 361 fimdscdeli peylnfirgv vdsedlplni sremlqqski lkvirknivk kclelfsla
 421 edkenykkfy eafsknlklg ihedstnrrr lsellryhts qsgdemtsls eyvsrmketq
 481 ksiyyitges keqvansafv ervrkrgfev vymtepidey cvqqlkefdg kslvsvtkeg
 541 lelpdedeek kkmeeskakf enlcklmkei ldkkvekvti snrlvssspcc ivtstygwta
 601 nmerimkaqa lrdnstmgym makkhleinp dhpietlrq kaeadkndka vndlvvllfe
 661 tallssgfsl edpqthsnri yrmiklgli dedevtaeep saavpdeipp legdedasrm
 721 eevd

HSP 84 (Human)
SEQ ID NO:5

1 mpeevhhgee evetfafqae iaqlmsliin tfysnkeifl relisnasda ldkiryeslt
 61 dpskldsgke lkidiipnpq ertltlvdtg igmtkadlin nlgtiaksgt kafmealqag
 121 adismigqfg vgfysaylva ekvvvitkhn ddegyawess aggsftvrad hgepigrgtk
 181 vilhikedqt eyleerrvke vvkkhsqfig ypitlyleke rekeisddea eeekgekeee
 241 dkdedeekpki edvgsdeedd sgdkkkktk kikekyidqe elnktpiwt rnpdditqee
 301 ygefyksltn dwedhlavkh fsveggolefr allfiprrap fdlfenkkkk nniklyvrrv
 361 fimdscdeli peylnfirgv vdsedlplni sremlqqski lkvirknivk kclelfsla
 421 edkenykkfy eafsknlklg ihedstnrrr lsellryhts qsgdemtsls eyvsrmketq
 481 ksiyyitges keqvansafv ervrkrgfev vymtepidey cvqqlkefdg kslvsvtkeg
 541 lelpdedeek kkmeeskakf enlcklmkei ldkkvekvti snrlvssspcc ivtstygwta
 601 nmerimkaqa lrdnstmgym makkhleinp dhpietlrq kaeadkndka vndlvvllfe
 661 tallssgfsl edpqthsnri yrmiklgli dedevaaeep naavpdeipp legdedasrm
 721 eevd

HSP 86 (Mouse)
SEQ ID NO:6

1 mpeetqtqdq pmeeeevetf afqaeiaqlm sliintfysn keiflrelis nssaldkir
 61 yesltdpskl dsgkelhnl ipskqdrtlt ivdtgigmkt adlinnlgti aksgtkafme
 121 alqagadism igqfvvgfys aylvaekvtv itkhnddeqy awessagsf tvrtdtgepm
 181 grgtkvilh1 kedqteylee rrikeivkhh sqfigypitl fvekerdkev sddeaeekee
 241 keekekeek esddkpeied vgsdeeeeek kdgdkkkkk ikekyidqe lnktkpwiwr
 301 npdditneey gefykslnd weehlavkhf sveggolefra llfprrapf dlfenrkkkn
 361 niklyvrrvf imdnceelip eylnfirgvv dsedlplnis remlqqskil kvirknlvkk
 421 clelfelae dkenykkfy qfskniklgi hedsqrkkl sellryytsa sgdemvs1kd
 481 yctrmkengk hiyfitgetk dqvansafve rlrkhglevi ymipeideyc vqqlkefegk
 541 tlsvtkegl elpedeekk kqeeektkfe nlckimkdil ekkvekvvs nrltspcci
 601 vtstygtan merimkaqal rdnstmgyma akkhleinpd hsietlrqk aeadkndksv
 661 kdlvillyet allssgfsle dpqthanriy rmiklgli dedptvddts aavteemppl
 721 egdddttsrme evd

HSP 86, HSP 60 (Human)

SEQ ID NO:7

1 mlrlptvfrq mrpvsrvlap hltrayakdv kfgadaralm lqgvdllada vavtmgpkgr
61 tvieeqswgs pkvtkgvttv aksidlkdःy knigaklvqd vanntneeag dgtttatvla
121 rsiakegfek iskganvei rrgvmlavda viaelkkqsk pvtpeeiaq vatisangdk
181 eigniisdam kkvggrkvit vkgdktlnde leieegmkfd rgyispyfin tskgqkcefq
241 dayvllsekk issiqsivpa leianahrkp lvviaedvdg ealstlvlnr lkvgloqvvav
301 kapgfgdnrk nqlkdmaiat ggavfgeegl tlnledvqph dlkvgeviv tkddamllkg
361 kgdkaqiekri iqeiiieqldv ttseyekekl nerlaklsdg vavlkgvgtts dvevnekdkdr
421 vtdalnatra aveegivlgg gcallrcipa ldslnpaned qkigieikr tlkipamtia
481 knagvegsli vekimqsse vgydamagdf vnmvekgiid ptkvvrtall daagvasllt
541 taevvvteip keekdpgmga mgggmgggmagg gmf

L-plastin (Human)

SEQ ID NO:8

1 margsvsdee mmelreafak vdtdgngyis fnelndlfka acplplpgyrv reitenlmat
61 gdldqdgris fdefikifhg lkstdvaktf rkainkkegi caiggseqs svgtqhsyse
121 eekyafvnwi nkalendpdc rhvipmnpt ndlfnavgdg ivlckminls vpdtiderti
181 nkkkltpfti genlnlalns asaigchvvn igaedlkegk pylvlglwq vikiglfadi
241 elsrnealia llregesled lmklspoeell lrwanyhlen agcnkignfs tdikdskayy
301 hleqvapkdg deegvpavvi dmsglrekdd igraecmlqq aerlgcrqfv tatdvvrgnp
361 klnlafianl fnrypalhkp enqdidwgal egetreertf rnwmnslgvn prvhlysd1
421 sdalvifqly ekikvpvdwn rvnkppypkl ggnmkklenc nyavelgknq akfslvgigg
481 qdlnegnrtl tlaliwqlmr rytnileei gggqkvnddi ivnwvnetlr eaekssiss
541 fkdpkistsl pvldlidaiq pgsinydl1k tenlnddekl nnakyaisma rkigarvyal
601 pedlhevnpk mvmtvfaclm gkgmkrv

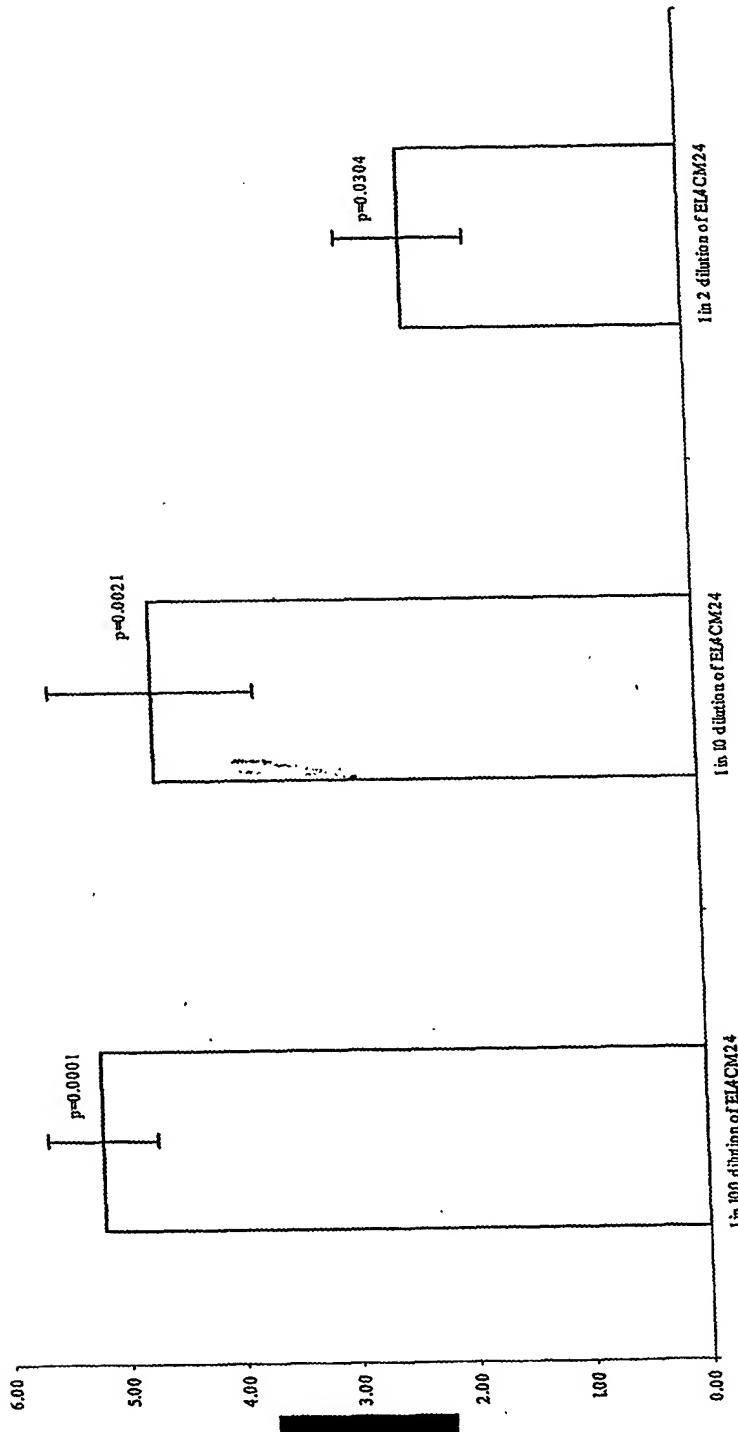
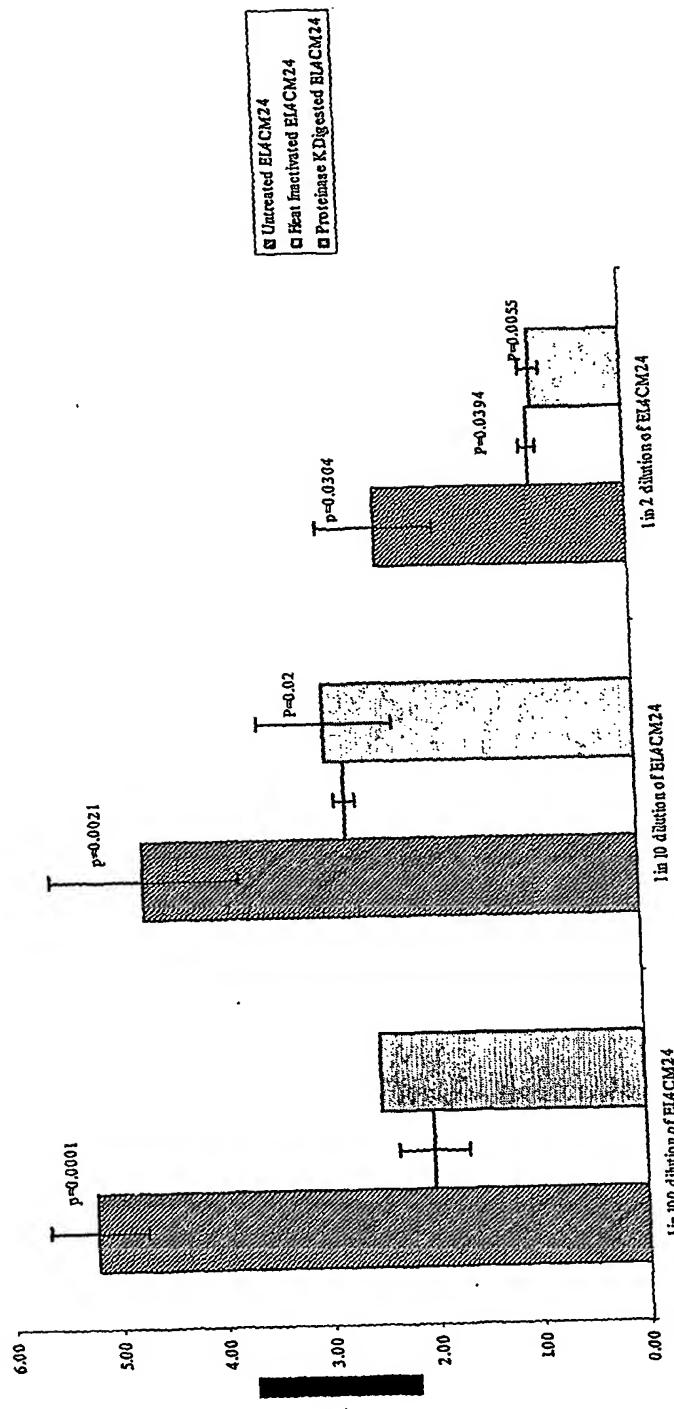
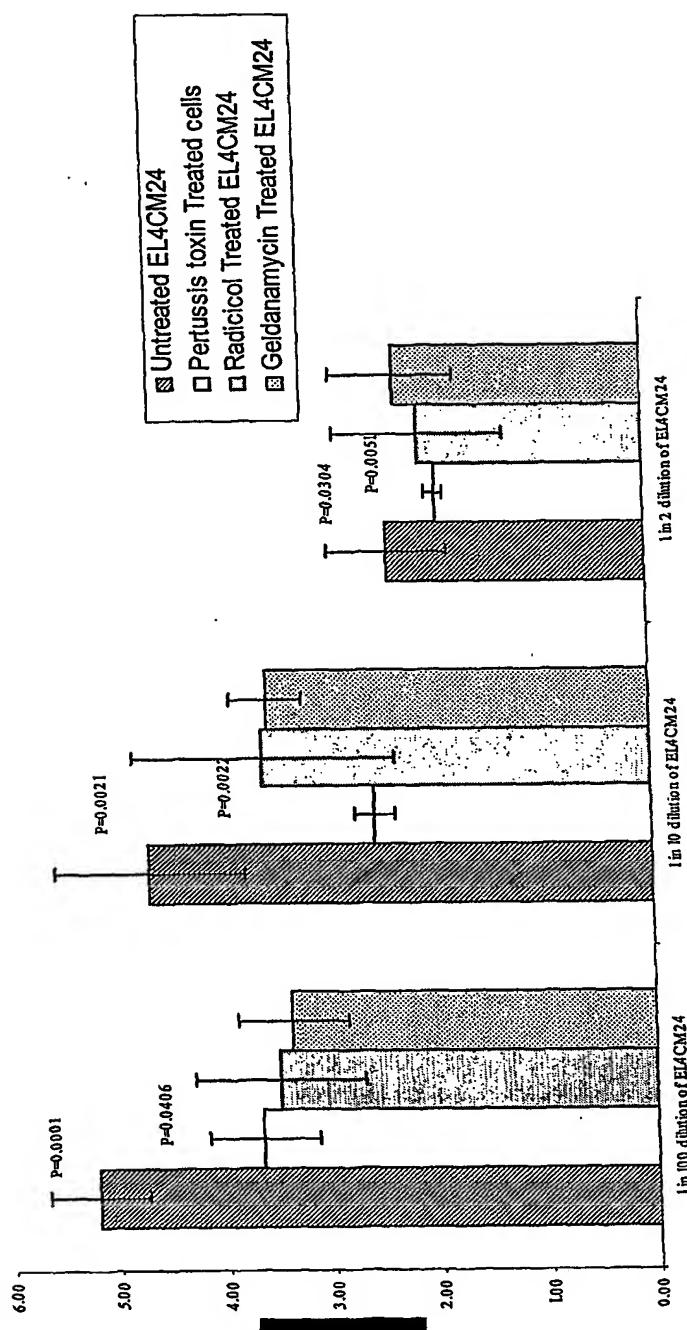
FIG. 2**EL4 Conditioned Media Repels T cells *in vitro***

FIG. 3

Heat Inactivation and Proteinase K Digestion of EL4CM24

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FIG. 4**Use of Specific Inhibitors**

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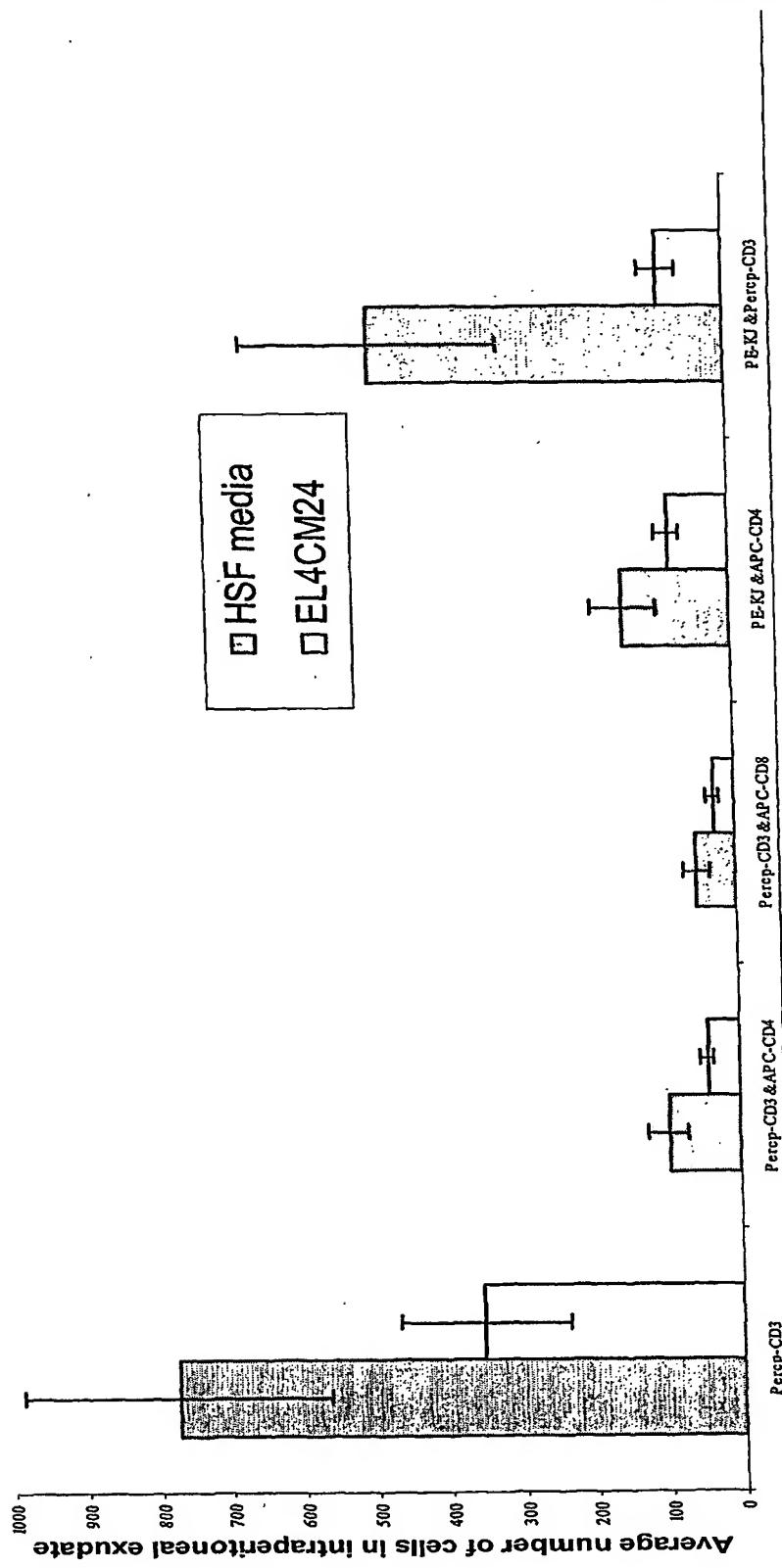
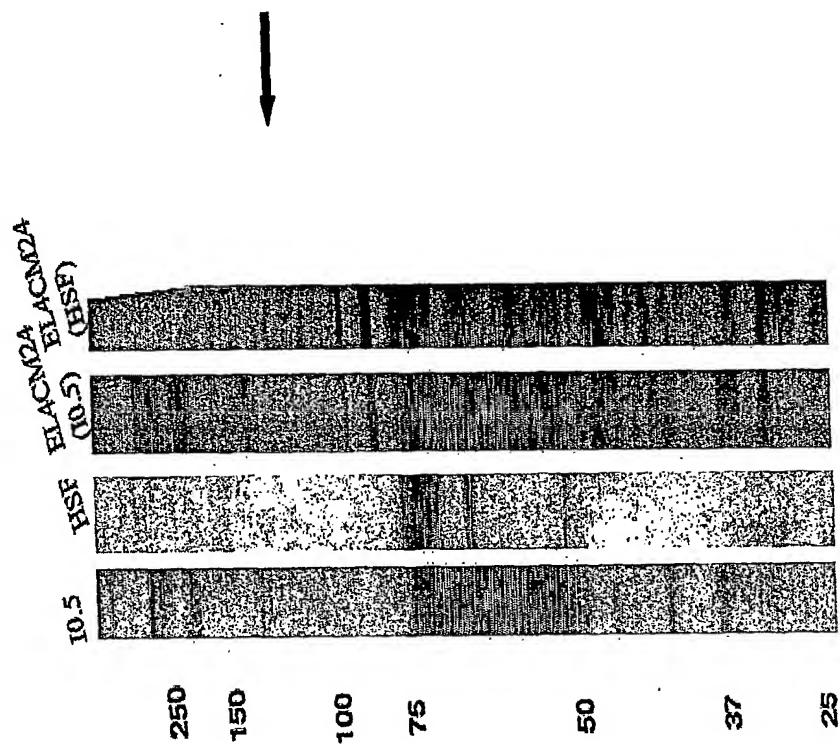
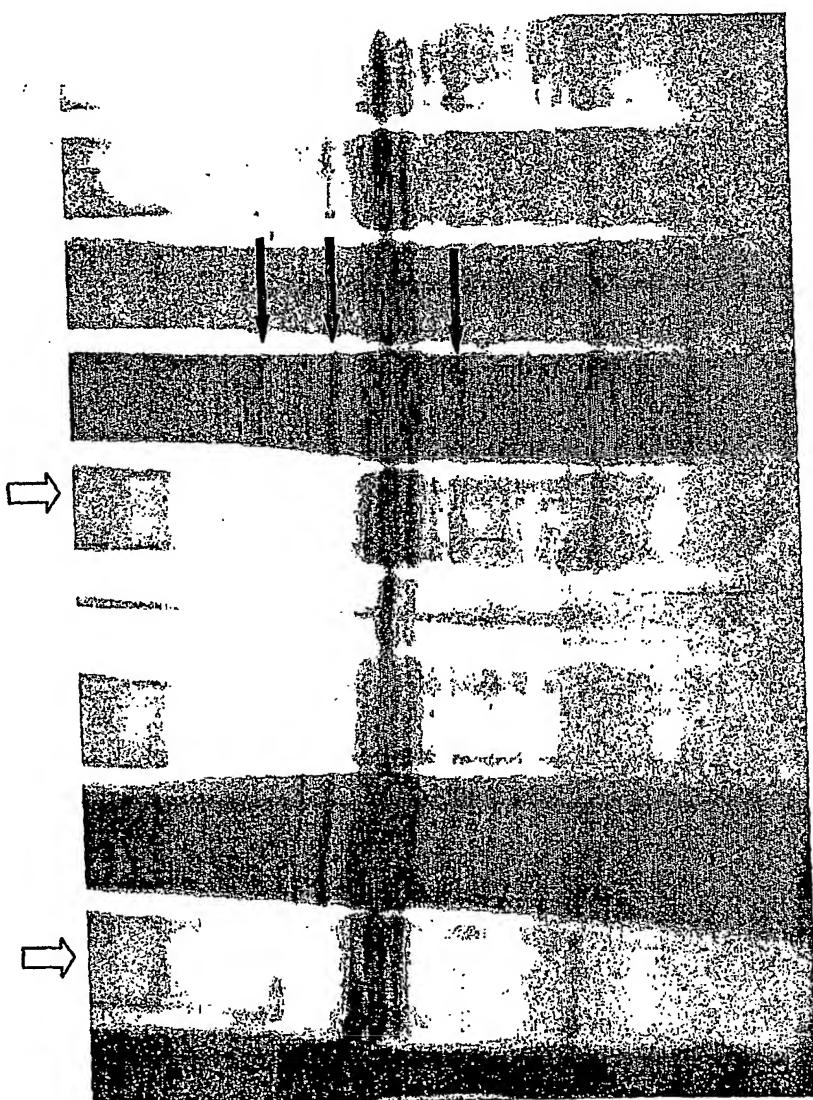
FIG. 5**EL4 Conditioned Media Repels T cells *in vivo*****Best Available Copy**

FIG. 6**EL4CM24 SDS PAGE**

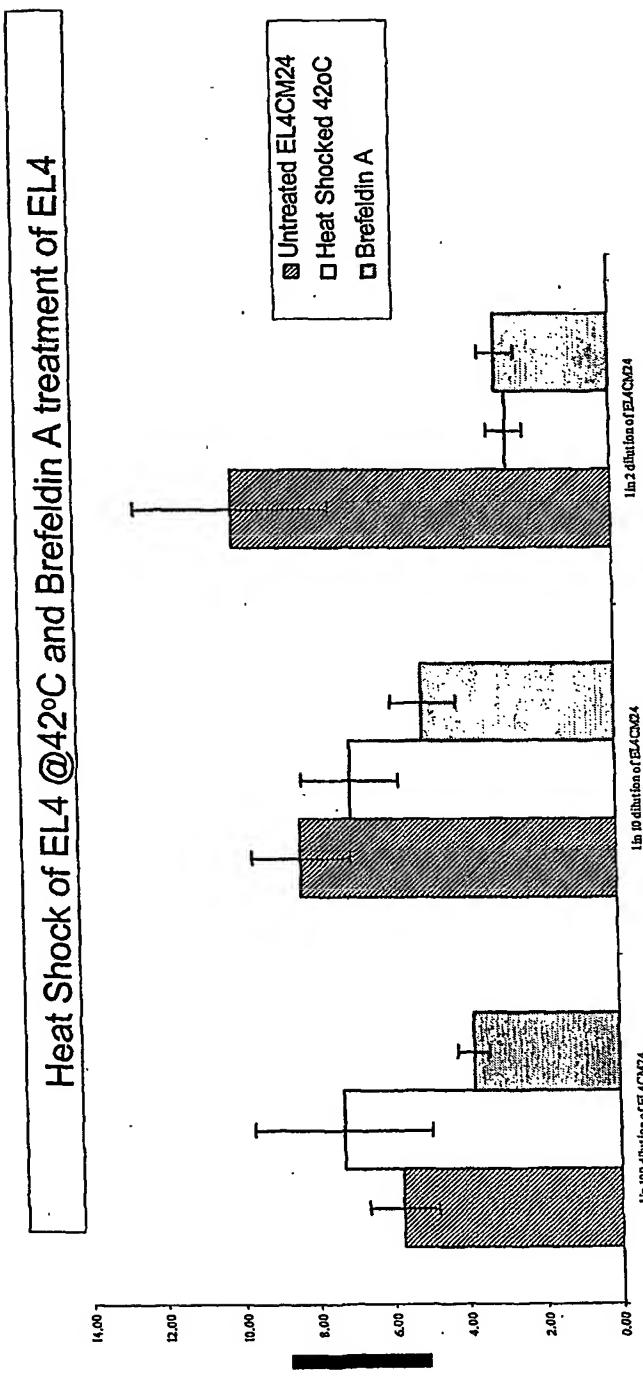
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FIG. 7

Ion Exchange Chromatography

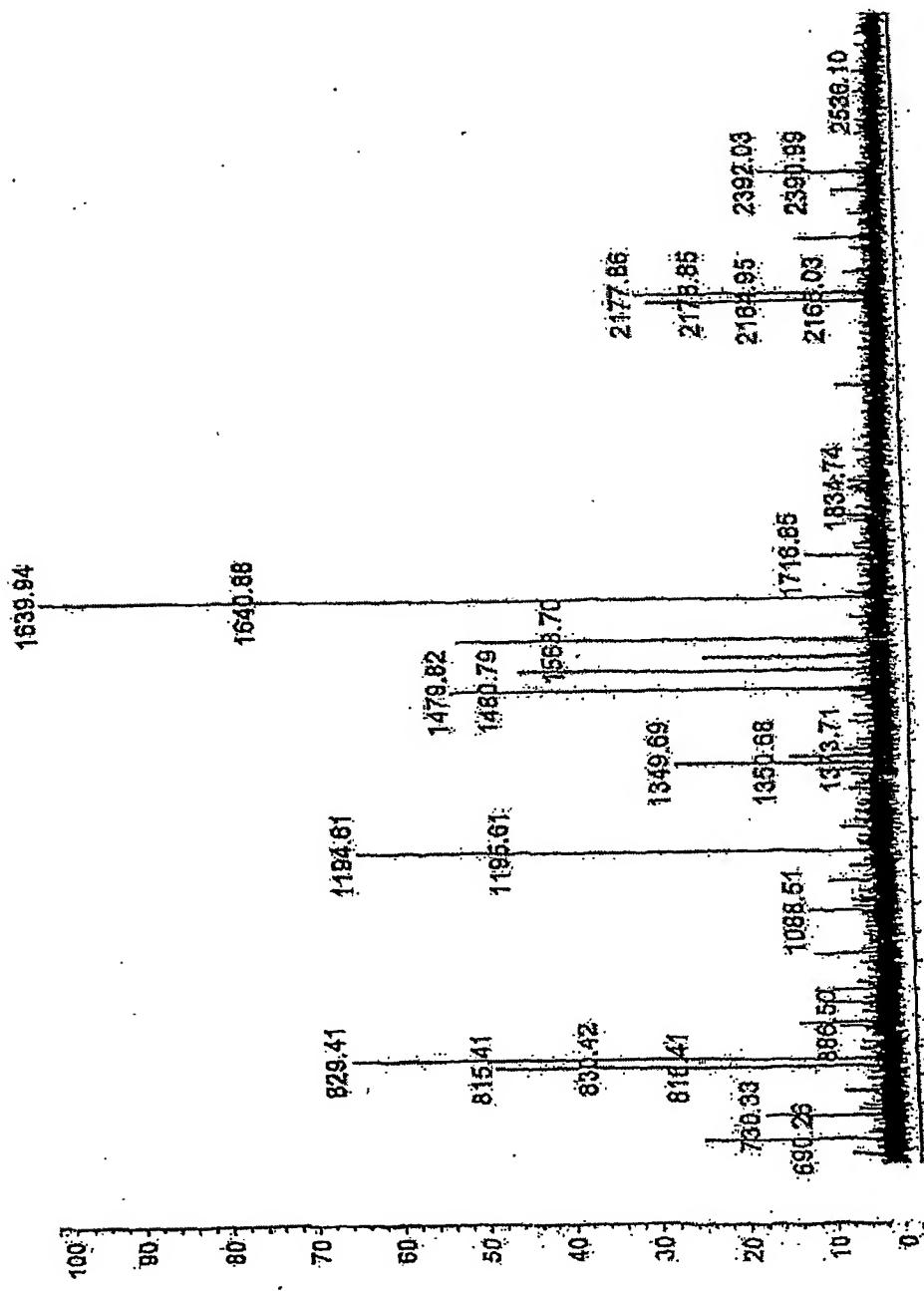


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FIG. 8

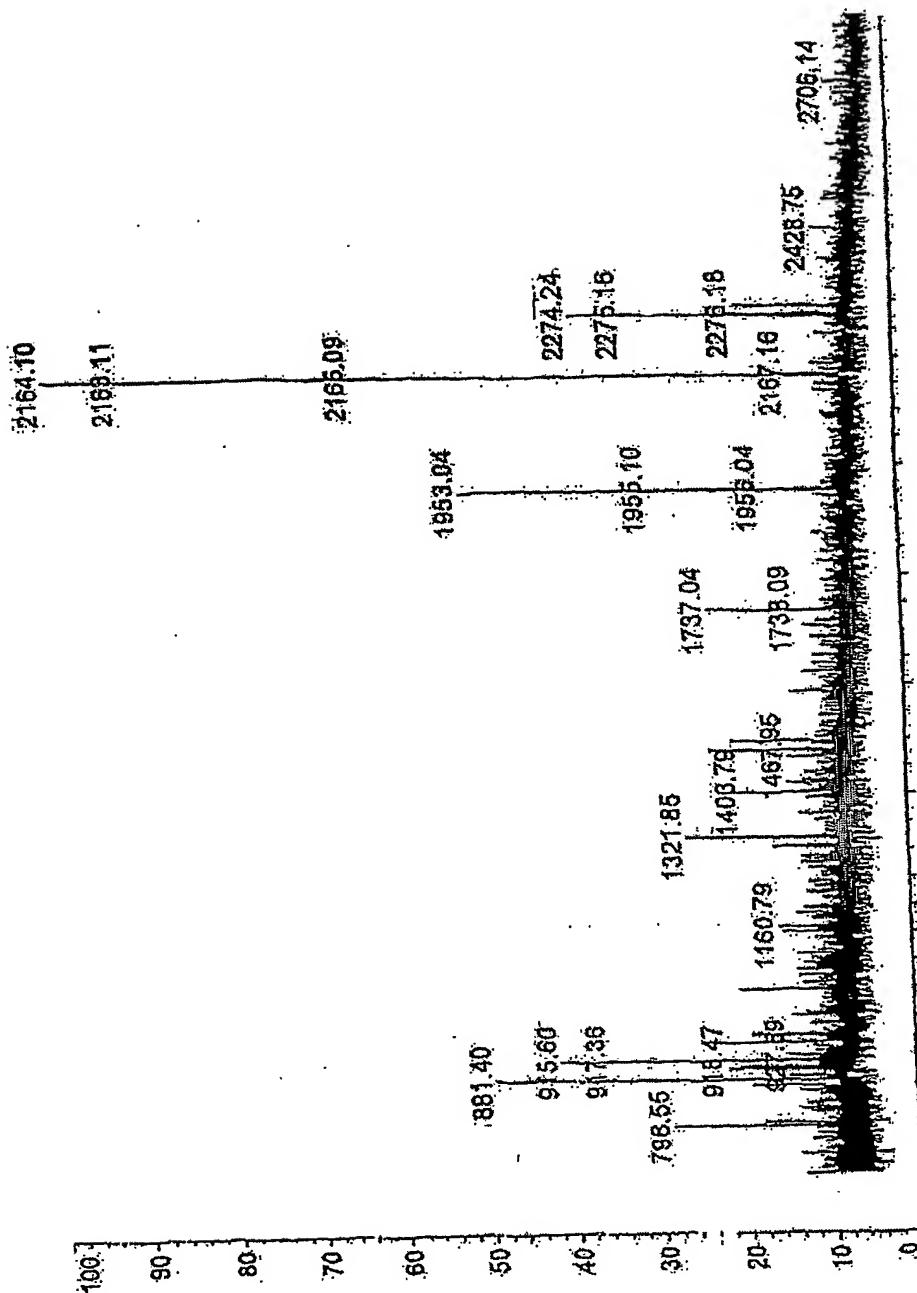
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FIG. 9



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FIG. 10



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FIG. 11

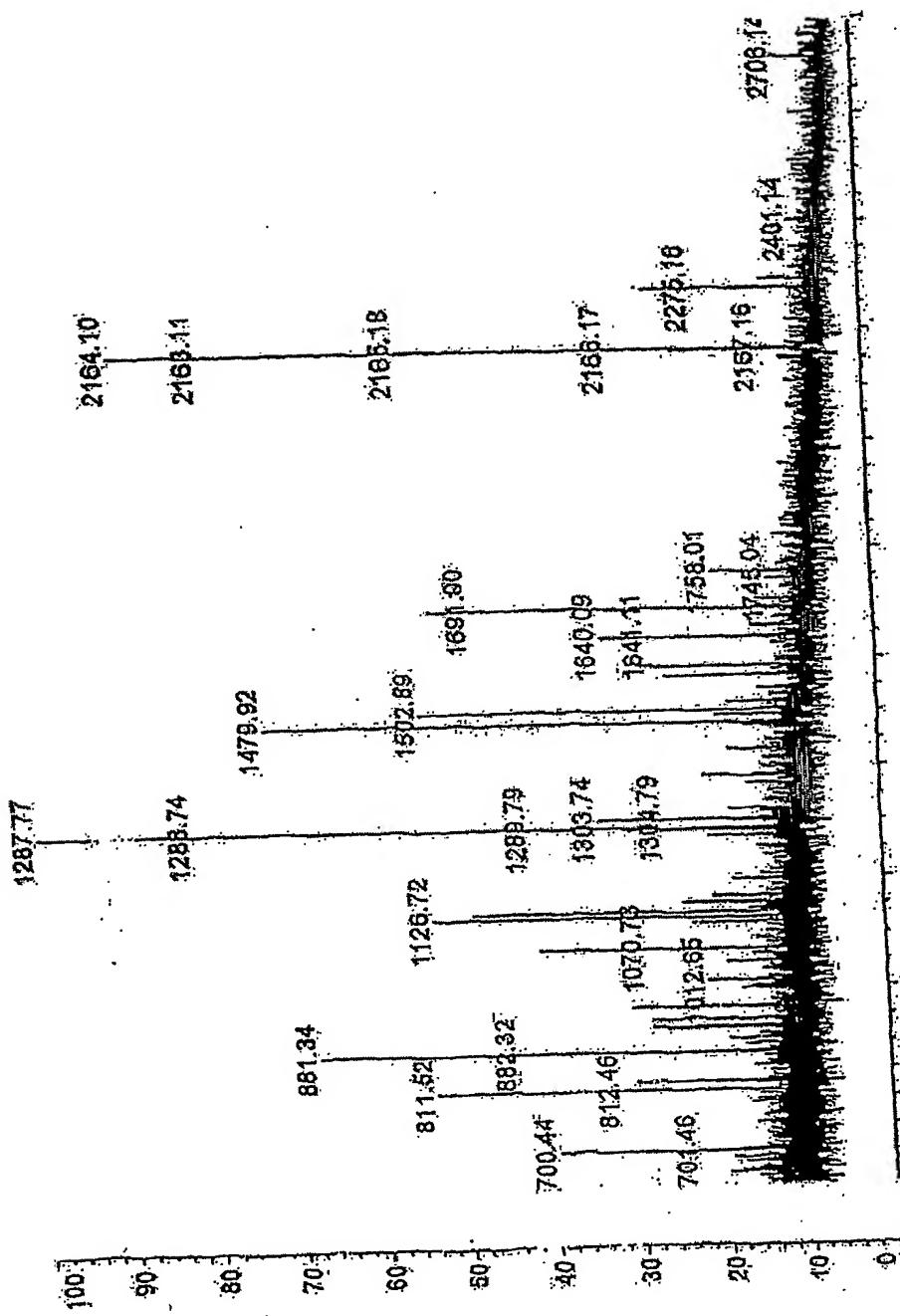


FIG. 12A

MS-Fit Search Results

Press Stop on your browser if you wish to abort this MS-Fit search prematurely.

Sample ID (comment): Magic Bullet digest

Database searched: NCBI nr. 121002

Molecular weight search (1000 - 100000 Da) selects 1195692 entries.

Full pI range: 1247039 entries.

Species search (MAMMALS) selects 197947 entries.

Combined molecular weight, pI and species searches select 186900 entries.

MS-Fit search selects 407 entries (results displayed for top 4 matches):

Considered modifications: (Peptide N-terminal Glu to pyroGlu) Oxidation of M | Protein N-terminal Acetylated |

Peptides to Match	Min. # Mass Tolerance (+/-)	Peptide Masses are monoisotopic	Digest Used	Max. # Missed Cleavages	Cysteines Modified by acrylamide	Peptide N-terminus Hydrogen (H)	Peptide C-terminus Free Acid (O, H)	Input # Peptides Masses
4	150.000 ppm		Trypsin	1				15

Result Summary

Rank	MOWSE Score	# (%) Masses Matched	Protein MW (Da)/pI	Species	NCBI nr. 121002 Accession #	Protein Name
1	7.07e+003	8/15 (53%)	81963.2 / 4.99	EQUUS CABALLUS	<u>20177936</u>	heat shock protein 90 beta
2	6.91e+003	8/15 (53%)	83264.6 / 4.97	HOMO SAPIENS	<u>20149594</u>	Unknown (protein for MGC:1138)
3	6.79e+003	8/15 (53%)	84843.9 / 5.26	HOMO SAPIENS	<u>11277141</u>	hypothetical protein
4	2.25e+003	7/15 (46%)	83326.8 / 5.06	RATTUS SP.	<u>1346320</u>	heat shock protein 90; hsp90

Detailed Results

1. 8/15 matches (53%), B1963.2 Da, pI = 4.99. Acc. # 20177936. EQUUS CABALLUS. heat shock protein 90 beta.

m/z	MR ⁺	Delta ppm	start and end	Peptide Sequence	Modifications
689.3000	689.3946	-137.2410	570	575 (K)YVTISN(R)L	
829.4100	829.5300	-144.6615	323	329 (R)ALLFIPR(R)	
891.3500	891.4252	-84.4094	421	427 (K)Q(E)YARKK(N)	
1194.6100	1194.6483	-32.0277	65	74 (K)(W)IPNHOER(T)	
1348.6900	1348.6650	18.5557	312	322 (K)RFSVCGOLEF(I)(A)	
1513.7800	1513.7862	-4.1036	371	384 (R)GVVDSEDLPLNISQ(R)	
2176.8600	2176.9457	-39.3681	449	467 (R)YHTSQSCDEMTSLSQEVYVSR(M)	
2390.9900	2391.1832	-80.4096	474	494 (K)SIYYITGESKEQVANSATVER(V)	

7 unmatched masses: 730.3300 815.4100 1479.8200 1537.7700 1567.7000 1639.9400 1715.8900

The matched peptides cover 13% (95/713 AA's) of the protein.
Coverage Map for This Hit (MS-Digest index #): 1205701

FIG. 12B

2. 8/15 matches (53%), 815.4100 Ox, pI = 4.97, Acc. # 20149394 HOMO SAPIENS, Unknown protein for MAC:1135.

m/z	MH ⁺	Delta ppm	start end	Peptide Sequence	Modifications
689.3000	689.3946	-137.2410	578 583	(Q)YVTSNHR(L)	
829.4100	829.5300	-144.6415	331 337	(R)ALLFIPPR(R)	
891.3500	891.4252	-84.4094	439 435	(K)EYFAESK(N)	
1194.6100	1194.6473	-32.0277	73 82	(K)DILPFNPDE(R)	
1348.6900	1348.6650	18.5557	320 330	(K)HISVEGOLPFR(A)	
1513.7800	1513.7862	-4.1036	379 392	(R)GVVVDSEPLNIS(R)	
2176.8600	2176.9457	-39.3681	457 475	(R)VHTSOSQHMTSLSEYVSR(M)	
2390.9900	2391.1832	-80.8096	482 502	(K)SIVVITGKGSKEOVANSAEVK(V)	

7 unmatched masses: 730.3100 815.4100 1479.8200 1537.7700 1567.7000 1639.9400 1715.8900

The matched peptides cover 13% (93/724 AA's) of the protein.
Coverage Map for This Hit (MS-Digest Index #: 137455).

3. 8/15 matches (53%), 815.4100, pI = 5.26, Acc. # 11277141, HOMO SAPIENS, hypothetical protein

m/z	MH ⁺	Delta ppm	start end	Peptide Sequence	Modifications
689.3000	689.3946	-137.2410	578 583	(Q)YVTSNHR(L)	
829.4100	829.5300	-144.6415	331 337	(R)ALLFIPPR(R)	
891.3500	891.4252	-84.4094	439 435	(K)EYFAESK(N)	
1194.6100	1194.6473	-32.0277	73 82	(K)DILPFNPDE(R)	
1348.6900	1348.6650	18.5557	320 330	(K)HISVEGOLPFR(A)	
1513.7800	1513.7862	-4.1036	379 392	(R)GVVVDSEPLNIS(R)	
2176.8600	2176.9457	-39.3681	457 475	(R)VHTSOSQHMTSLSEYVSR(M)	
2390.9900	2391.1832	-80.8096	482 502	(K)SIVVITGKGSKEOVANSAEVK(V)	

7 unmatched masses: 730.3100 815.4100 1479.8200 1537.7700 1567.7000 1639.9400 1715.8900.

The matched peptides cover 12% (93/737 AA's) of the protein.
Coverage Map for This Hit (MS-Digest Index #: 1101246).

4. 7/15 matches (46%), 813.612 Da, pI = 5.06, Acc. # 1341620, RATTUS SP., heat shock protein 90; hsp90.

m/z	MH ⁺	Delta ppm	start end	Peptide Sequence	Modifications
689.3000	689.3946	-137.2410	578 583	(Q)YVTSNHR(L)	
829.4100	829.5300	-144.6415	331 337	(R)ALLFIPPR(R)	
891.3500	891.4252	-84.4094	439 435	(K)EYFAESK(N)	
1194.6100	1194.6473	-32.0277	73 82	(K)DILPFNPDE(R)	
1348.6900	1348.6650	18.5557	320 330	(K)HISVEGOLPFR(A)	
1513.7800	1513.7862	-4.1036	379 392	(R)GVVVDSEPLNIS(R)	
2176.8600	2176.9457	-39.3681	457 475	(R)VHTSOSQHMTSLSEYVSR(M)	
2390.9900	2391.1832	-80.8096	482 502	(K)SIVVITGKGSKEOVANSAEVK(V)	

8 unmatched masses: 730.3100 815.4100 1194.6100 1479.8200 1537.7700 1567.7000 1639.9400 1715.8900.

MS-Tag Search Results

Sample ID (filename): ApoA1_1_040AKPVLEDLN
Database searched: NCBI nr 111002.
Full Molecular Weight range: 1347039 entries.
Full of range: 1347039 entries.
Species search (MAMMALIA) selects 191947 entries.
Number of sequences passing through parent score filter: 4253
MS-Tg Search selects 7 entries (results displayed for top 3 matches).

Pancreas mass: 1194.6100 (+/- 0.2000 Da)
Fragment ions used in search: 178.3, 212.0, 323.20, 342.61, 355.43, 512.43, 523.50, 616.31, 713.44, 740.58, 366.93 (+/- 0.50 Da)

Ion types Considered: a b c y z b'

Search Mode	Unmatched Ions	Peptide Masses	Digest	Mass & Modified Cysteines	Peptides
Identify	1	monoprotic	Tryptic	{	N-terminal C-terminal Hydrogen (H) : Free Acid (O H)

Result Summary

Rank	Unmatched Ions	Sequence	Calc'd. MH ⁺ (Da)	Error (Da)	Protein MH ⁺ (Da)	Species	NCBI ID/22202	Protein Name
1	0/11	(K)DILPFNPDE(R)	1194.6483	-0.0383	1194.6100	MOUSE	121611	Heat shock protein HSP 90-beta (HSP 60) (Tumour specific transplantation 42 kDa antigen) (TSTA)
1	0/11	(K)DILPFNPDE(R)	1194.6483	-0.0383	1194.6100	MUS MUSCULUS	661005	heat shock protein, 64 kDa
1	0/11	(K)DILPFNPDE(R)	1194.6483	-0.0383	1194.6100	HOMO SAPIENS	1341620	heat shock protein beta

FIG. 12C

Detailed Results

Rank	Unmatched Ions	Sequence	MH ⁺ Calculated (Da)	MH ⁺ Error (Da)	Protein MW(Da)/pI	Species	NCBI nr:121002 Accession #	MS-Digest Index #	Protein Name				
1	0/11	(K)DILPNPOERT(T)	1194.6483	-0.0383	83325.7 / 4.97	MOUSE	113681	318176	heat shock protein HSP 90-beta (HSP 84) (Tumor specific transplantation 84 kDa antigen) (TSTA)				
	D/17	(K)DILPNPOERT(T)	1194.6483	-0.0383	83361.1 / 5.03	MUS MUSCULUS	6680305	583990	heat shock protein, 14 kDa 1				
		Fragment-Ion (m/z)	175.31	212.00	229.70	342.62	355.41	512.43	529.50	626.31	723.44	740.58	966.73
		Ion-type	y ₁	NP	b ₁	b ₂	PQE	y ₄ -NH ₃	y ₄	y ₅ -NH ₃	y ₆ -NH ₃	y ₆	y ₁
		Delta D _s	0.19	-0.10	0.08	0.42	0.27	0.18	0.23	0.02	0.10	0.21	0.19
		Fragment-Ion (m/z)	175.31	211.00	219.10	342.62	355.41	512.43	529.50	626.31	723.44	740.58	966.73
		Ion-type	y ₁	NP	b ₂	b ₃	PQE	y ₄ -NH ₃	y ₄	y ₅ -NH ₃	y ₆ -NH ₃	y ₆	y ₁
		Delta D _s	0.19	-0.10	0.08	0.42	0.27	0.18	0.23	0.02	0.10	0.21	0.19
		0/11	(K)DILPNPOERT(T)	1194.6483	-0.0383	140664 / 4.64	HOMO SAPIENS	1151110	587097	heat shock protein 68.			
		Fragment-Ion (m/z)	175.31	211.00	219.10	342.62	355.41	512.43	529.50	626.31	723.44	740.58	966.73
		Ion-type	y ₁	NP	b ₂	b ₃	PQE	y ₄ -NH ₃	y ₄	y ₅ -NH ₃	y ₆ -NH ₃	y ₆	y ₁
		Delta D _s	0.19	-0.10	0.08	0.42	0.27	0.18	0.23	0.02	0.10	0.21	0.19

MS-Tag Search Results

Sample ID (cont'd): Apo A-1:1040 AKPVLEDLR
 Database searched: NCBI nr:121002
 Molecular weight search (1000 - 100000 Da) selects 1195692 entries.
 Full pI range: 1147039 entries.
 Species search (MAMMALS) selects 197947 entries.
 Combined molecular weight, pI and species searches select 186900 entries.
 Number of sequences passing through parent mass filter: 4989
 MS-Tag search selects 18 entries (results displayed for top 3 matches).

Parent mass: 815.4100 (+/- 0.7000 Da)
 Fragment-Ion used in search: 185.76, 235.27, 272.34, 298.32, 354.45, 371.53, 417.39, 445.25, 518.35 (+/- 0.50 Da)

Ion Types Considered: a b By n h I

Search Mode	Max. # Unmatched Ions	Peptide Masses	Digest	Max. # Missed Cleavages	Cysteines Modified by	Peptide N terminus	Peptides C-terminal
Identify	1	monoktopic, Trypsin	1		acrylamide	Hydrogen (H)	Free Acid (OH)

Result Summary

#	Rank	Unmatched Ions	Sequence	MH ⁺ Calculated (Da)	MH ⁺ Error (Da)	Protein MW(Da)/pI	Species	NCBI nr:121002 Accession #	Protein Name
1	0/9	(R)AILFYPR(R)	815.5143 -0.1043	75541.0 / 5.18	MUS MUSCULUS	20882555	similar to heat shock protein 68		
1	0/9	(R)AILFYPR(R)	815.5143 -0.1043	84674.2 / 4.94	HOMO SAPIENS	123678	90 kDa heat-shock protein (AA 1-732)		
1	0/9	(K)AILFYPR(R)	815.5143 -0.1043	57068.0 / 6.38	HOMO SAPIENS	12804541	hypothetical protein LOC63929		

Detailed Results

#	Rank	Unmatched Ions	Sequence	MH ⁺ Calculated (Da)	MH ⁺ Error (Da)	Protein MW(Da)/pI	Species	NCBI nr:121002 Accession #	MS-Digest Index #	Protein Name	
1	0/9	(R)AILFYPR(R)	815.5143 -0.1043	75541.0 / 5.18	MUS MUSCULUS	20882555	similar to heat shock protein 68				
1	0/9	(R)AILFYPR(R)	815.5143 -0.1043	84674.2 / 4.94	HOMO SAPIENS	123678	90 kDa heat-shock protein (AA 1-732)				
		Fragment-Ion (m/z)	185.76	255.27	272.34	298.32	354.45	371.53	417.39	445.25	518.35
		Ion-type	b ₁	y ₂ -NH ₃	y ₃	b ₂	y ₄ -NH ₃	y ₃	a ₄	y ₄	
		Delta D _s	0.13	0.12	0.17	0.11	0.24	0.29	0.10	-0.03	0.04
		Fragment-Ion (m/z)	185.76	255.27	272.34	298.32	354.45	371.53	417.39	445.25	518.35
		Ion-type	b ₁	y ₂ -NH ₃	y ₃	b ₂	y ₄ -NH ₃	y ₃	a ₄	y ₄	
		Delta D _s	0.13	0.12	0.17	0.11	0.24	0.29	0.10	-0.03	0.04
	0/2	(K)AILFYPR(R)	815.5143 -0.1043	57068.0 / 6.38	HOMO SAPIENS	12804541	171353	hypothetical protein LOC63929			
		Fragment-Ion (m/z)	185.76	255.27	272.34	298.32	354.45	371.53	417.39	445.25	518.35
		Ion-type	b ₁	y ₂ -NH ₃	y ₃	b ₂	y ₄ -NH ₃	y ₃	a ₄	y ₄	
		Delta D _s	0.13	0.12	0.17	0.11	0.24	0.29	0.10	-0.03	0.04

FIG. 13A

MS-Fit Search Results

Sample ID (comment): ntagic Bullet digest
 Database searched: NCBI nr. \$1403
 Molecular weight search (1000 - 20000 Da) selects 1421445 entries.
 Full pI range: (432416 entries).
 Species search (HUMAN RODENT) selects 224838 entries.
 Combined molecular weight, pI and species searches selects 222557 entries.
 MS-Fit search selects 5 entries (results displayed for top 3 matches).
 Considered modifications: [Peptide N-terminal C-terminal (o) pyroGlu] Oxidation of M (Protein N-terminus Acetylated)

Peptide Min. # Peptides to Match	Peptide Mass Tolerance (+-) 7 150.000 ppm	Peptide Masses are monoisotopic	Digest Used Trypsin	Max. # Mixed Cleavages	Cysteines Modified by acrylamide	Peptide N-terminus Hydrogen (H)	Peptide C-terminus Free Acid (O H)	Input # Peptide Masses 13
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Result Summary

Rank	MOWSE Score	# (%) Matched	Protein mW (Da)/pI	Species	NCBI nr. \$1403 Accession #	Protein Name
1	1.81e+003	7/13 (53%)	94057.0 / 5.13	RATTUS NORVEGICUS	24025637	ischemia responsive 94 kDa protein
2	449	7/13 (53%)	94081.1 / 5.13	MUS MUSCULUS	13277753	heat shock protein 4
2	449	7/13 (53%)	94133.1 / 5.15	MUS MUSCULUS	6680301	apg-2

Detailed Results

1. 7/13 matches (53%), 94057.0 Da, pI = 5.13, Acc. # 24025637, RATTUS NORVEGICUS, ischemia responsive 94 kDa protein.

m/z submitted matched	Mr ppm	Delta start cod	Peptide Sequence	Modifications:
798.5500	798.4514	123.4493	431 436 (K)QVILTEVK(K)	
949.6100	949.5219	92.7425	62 69 (K)NTVOGEKRF(F)	
1323.8500	1327.7216	104.7200	222 234 (K)QVILATAFDITLGGR(K)	
1402.7800	1402.6313	196.0213	619 629 (R)QNAVEEYVVEMR(D)	
1495.8400	1495.7029	91.6785	20 33 (R)AGGQETIANEYSDR(C)	
1736.0700	1735.9271	87.3407	391 405 (R)EGSITDVVPPYFISLR(W)	
1953.0400	1952.8336	105.6759	406 422 (R)WNSPAEEGSSDCEVFPK(N)	

1 unmatched masses: 915.6000 917.3600 1305.8400 1478.8800 1587.9500 1624.0300

The matched peptides cover 10% (84/840 AA's) of the protein.
 Coverage Map for This Hit (MS-Digest Index #): [787619](#)

7/13 matches (53%), 94081.1 Da, pI = 5.13, Acc. # 13277753, MUS MUSCULUS, heat shock protein 4

FIG. 13B

m/z	MH ⁺	Delta ppm	start	end	Peptide Sequence	Modifications
submitted	matched					
798.5500	798.4514	123.4893	431	436	(K)YLTIFYR(K)	
949.6100	949.5219	92.7425	62	69	(K)NTVOGFKR(P)	
1305.8400	1305.7418	75.1849	670	680	(K)QVYVVDKLAELK(S)	
1321.8500	1321.7116	104.7200	222	234	(K)VLTATAFDITLGGR(K)	
1402.7800	1402.6313	106.0213	620	630	(K)NAVEEYVVYEMR(D)	
1495.8400	1495.7029	91.6785	20	33	(R)AGCIELTIANEYSDR(C)	
1736.0700	1735.9271	82.3407	391	405	(R)EFSITDVVVYPISLR(W)	

6 unmatched masses: 915.6000 917.3600 1478.8800 1587.9500 1624.0500 1953.0400

The matched peptides cover 9% (78/841 AA's) of the protein.

Coverage Map for This Hit (MS-Digest index #): 302745.

2. 7/13 matches (53%), 94133.1 Da, pI= 5.15, Acc. # 6680301, MUS MUSCULUS, spg.2..

m/z	MH ⁺	Delta ppm	start	end	Peptide Sequence	Modifications
submitted	matched					
798.5500	798.4514	123.4893	431	436	(K)YLTIFYR(K)	
949.6100	949.5219	92.7425	62	69	(K)NTVOGFKR(P)	
1305.8400	1305.7418	75.1849	670	680	(K)QVYVVDKLAELK(S)	
1321.8500	1321.7116	104.7200	222	234	(K)VLTATAFDITLGGR(K)	
1402.7800	1402.6313	106.0213	620	630	(K)NAVEEYVVYEMR(D)	
1495.8400	1495.7029	91.6785	20	33	(R)AGCIELTIANEYSDR(C)	
1736.0700	1735.9271	82.3407	391	405	(R)EFSITDVVVYPISLR(W)	

5 unmatched masses: 915.6000 917.3600 1478.8800 1587.9500 1624.0500 1953.0400

The matched peptides cover 9% (78/841 AA's) of the protein.

Coverage Map for This Hit (MS-Digest index #): 1139227.

FIG. 14A

MS-Fit Search Results

Sample ID (controll): Magic Bullet digest

Database searched: NCBI nr.51403

Molecular weight search (1000 - 100000 Da) selects 1372760 entries.

Full pI range: 1432416 entries.

Species search (HUMAN RODENT) selects 224838 entries

Combined molecular weight, pI and species searches select 211465 entries.

MS-Fit search selects 335 entries (result displayed for top 3 matches).

Considered modifications: [Peptide N-terminal C¹ in pyroGlu] Oxidation of M [Protein N-terminal Acetylated]

Peptide Min. # Peptides to Match	Max Masses (+-) 4	Peptide Masses are monoisotopic. 150,000 ppm	Digest Used: Trypsin	Max. #: Missed Cleavages 1	Cysteines Modified by acrylamide	Peptide N terminus Hydrogen (H)	Peptide C terminus Free Acid (O-H)	Input # Peptide Masses 17
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Result Summary

Rank	MOWSE Score	# (%) Matched	Protein MW (Da)/pI	Species:	NCBI nr.51403 Accession #	Protein Name
1	1.22e+005	11/17 (64%)	70149.7 / 5.20	MUS MUSCULUS	29840803	unnamed protein product
2	1.22e+005	11/17 (64%)	70163.8 / 5.24	MUS MUSCULUS	26326929	unnamed protein product
3	2.66e+004	10/17 (58%)	70201.8 / 5.28	MUS MUSCULUS	6679385	65-kDa macrophage protein

Detailed Results

11/17 matches (64%). 70149.7 Da, pI = 5.20, Acc #29840803, MUS MUSCULUS, unnamed protein product.

m/z submitted, matched	M(H) ⁺ ppm	Delta	start	end	Peptide Sequence	Modifications
700.4400	700.4146	36.2352	77	82	(K)VFTIGLK(S)	
811.5200	811.4136	131.0872	585	591	(K)YALSMAR(K)	
942.5800	942.5413	47.0831	442	449	(R)YNTXPPVPK(L)	
1069.7200	1069.6257	88.1285	264	272	(K)LSPFELLRLR(W)	
1126.7200	1126.6373	73.4015	433	441	(K)KVPVWDWNR(V)	
1135.7100	1135.6111	87.0474	348	357	(R)QEVATDVVR(G)	
1287.7700	1287.6268	111.2008	402	412	(R)NWVNNSLGVNPR(V)	
1502.8900	1502.7525	91.5194	166	178	(K)MINLSVFTDIDEN(T)	
1585.9400	1585.8477	58.1710	597	610	(R)VYALTEDLVEVNP(K)	
1689.9700	1689.8560	67.4478	473	488	(K)FSLVGIACQDINEGNR(T)	
1758.0100	1757.8744	77.1528	310	326	(K)GREGIPAVVVIDMSCLR(P)	

unmatched masses: 927.5400 964.6000 1478.8800 1479.9200 1567.8600 1640.0900

the matched peptides cover 19% (120/627 AA's) of the protein.

FIG. 14B

Coverage Map for This Hit (MS-Digest index #): 372729

2. 11/17 matches (64%). 70163.8 Da, pI = 5.24; Acc. # 26326929, MUS MUSCULUS, unnamed protein product.

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence	Modifications
700.4400	700.4146	36.2352	77	82	(K)VFHGLK(S)	
811.5200	811.4136	131.0872	585	591	(K)YALSMAR(K)	
942.5800	942.5413	41.0831	442	449	(R)VNKPYPK(L)	
1069.7200	1069.6257	88.1285	264	272	(K)SPFELLER(W)	
1126.7200	1126.6373	73.4015	433	441	(K)IKVPYDWR(V)	
1135.7100	1135.6111	87.0474	348	357	(R)QFVTATDVVR(G)	
1281.7700	1287.6268	111.2008	402	412	(R)NWMNSLGVNPR(V)	
1502.8900	1502.7525	91.5194	166	178	(K)MINLSVPDTIDEK(T)	
1585.9400	1585.8477	58.1710	597	610	(R)YVALPEDIVEVNPK(M)	
1689.9700	1689.8560	67.4478	473	488	(K)FSLVGLACQDLNEGNR(T)	
1758.0100	1757.8744	77.1528	310	326	(K)GDEEGIPAVVVIDMSCLR(E)	

6 unmatched masses: 927.5400 964.6000 1478.8800 1479.9200 1567.8600 1640.0900

The matched peptides cover 19% (120/627 AA's) of the protein.

Coverage Map for This Hit (MS-Digest index #): 1174311

3. 10/17 matches (58%). 70201.8 Da, pI = 5.28; Acc. # 6679385, MUS MUSCULUS, 65-kDa macrophage protein.

m/z submitted	MH ⁺ matched	Delta ppm	start	end	Peptide Sequence	Modifications
700.4400	700.4146	36.2352	77	82	(K)VFHGLK(S)	
811.5200	811.4136	131.0872	585	591	(K)YALSMAR(K)	
942.5800	942.5413	41.0831	442	449	(R)VNKPYPK(L)	
1069.7200	1069.6257	88.1285	264	272	(K)SPFELLER(W)	
1126.7200	1126.6373	73.4015	433	441	(K)IKVPYDWR(V)	
1135.7100	1135.6111	87.0474	348	357	(R)QFVTATDVVR(G)	
1281.7700	1287.6268	111.2008	402	412	(R)NWMNSLGVNPR(V)	
1502.8900	1502.7525	91.5194	166	178	(K)MINLSVPDTIDEK(T)	
1585.9400	1585.8477	58.1710	597	610	(R)YVALPEDIVEVNPK(M)	
1758.0100	1757.8744	77.1528	310	326	(K)GDEEGIPAVVVIDMSCLR(E)	

7 unmatched masses: 927.5400 964.6000 1478.8800 1479.9200 1567.8600 1640.0900 1689.9700

The matched peptides cover 16% (104/627 AA's) of the protein.

Coverage Map for This Hit (MS-Digest index #): 746520

FIG. 14C

MS-Tag Search Results

Sample ID (contingency): Apo A-1 1040 AKPVLEDDIX

Database searched: NCBIInv.51403

Molecular weight search (1000 - 200000 Da) selects 1421445 entries.

Full pI range: 493416 entries.

Species search (HUMAN / RODENT) selects 124838 entries.

Compound molecular weight, pI and species search select 122537 entries.

Number of sequences passing through parent mass filter: 3727

MS-Tag search selects 6 entries.

Parent mass: 1287.7100 (\pm 0.2000 Da)Fragments ions used in search: 175.00, 235.26, 301.46, 369.37, 432.69, 542.65, 633.34, 655.97, 742.67, 840.69 (\pm 0.70 Da)

Ion Types Considered: a b C y z

Search Modality	Max. Ion	Unmatched Peptides	Peptide Mass	Digest	Max. # Missed	Cysteines	Peptides Modified by	Peptides N-terminal	Peptides C-terminal
Monosaccharide	2	mono-saccharide	Trypsin	Urea	1		Acrylamide	Hydrogen (H)	Free Acid (O H)

Result Summary

Rank	# Unmatched Ions	Sequence	MET ^a Calculated	MH ^b Error	Protein MW (Da)/pI	Species	NCBIInv.51403 Accession #	MS-Digest Index #	Protein Name
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70288.8 / 5.19	HOMO SAPIENS	1117500	6A139H14.1 (lymphocyte cytosolic protein 1 (L-plastin))	
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70289.7 / 5.10	HOMO SAPIENS	1504985	lymphocyte cytosolic protein 1 (L-plastin)	
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70201.8 / 5.18	MUS MUSCULUS	6679385	63-KDa macrophage protein	
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70131.4 / 5.30	MUS MUSCULUS	12845863	unamed protein product	
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70149.7 / 5.24	MUS MUSCULUS	26326912	unamed protein product	
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70149.7 / 5.20	MUS MUSCULUS	29840803	unamed protein product	

Detailed Results

Rank	# Unmatched Ions	Sequence	MET ^a Calculated	MH ^b Error	Protein MW (Da)/pI	Species	NCBIInv.51403 Accession #	MS-Digest Index #	Protein Name
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70288.8 / 5.19	HOMO SAPIENS	8213500	6A139H14.1 (lymphocyte cytosolic protein 1 (L-plastin))	
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70289.7 / 5.10	HOMO SAPIENS	1504985	lymphocyte cytosolic protein 1 (L-plastin)	
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70201.8 / 5.18	MUS MUSCULUS	6679385	63-KDa macrophage protein	
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70131.4 / 5.30	MUS MUSCULUS	12843863	unamed protein product	
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70149.7 / 5.24	MUS MUSCULUS	16316922	unamed protein product	
1	1/11	(R)NWMNSLGVNPR(V)	1287.6268	0.1432	70149.7 / 5.20	MUS MUSCULUS	19840803	unamed protein product	

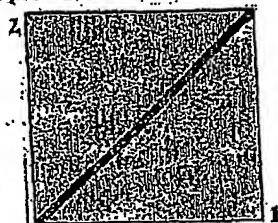
Fragmenet-Ion (m/z)	175.00	255.28	277.30	301.48	369.37	432.69	542.65	633.34	655.97	742.67	840.69
Ion-type	y ₁	y ₂ -NH ₂	y ₂	b ₂	y ₁ -NH ₂	b ₁	y ₁	y ₂	y ₆	y ₇	y ₁
Delta Da	+0.12	+0.13	+0.13	+0.33	+0.18	+0.57	+0.34	+0.09	+0.58	+0.21	+0.21

FIG. 15A

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4

Matrix [BLOSUM62] gap open: 11 gap extension: 1
 x_dropoff: 50 expect: 10.00 wordsize: 3 Filter

Sequence 1 gi|17865718 Heat shock protein HSP 90-beta (HSP 84) (HSP 90) Length 724 (1..724)
 Sequence 2 gi|72223 heat shock protein 84 - mouse Length 724 (1..724)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 1178 bits (304%) Expect = 0.0
 Identities = 616/724 (85%), Positives = 616/724 (85%)

Query: 1	MPXXXXXXXXXXTEFAQEIAQQLMSLIINTFYSNKEIFLRELITNASDALDKIRYESLT	60
Sbjct: 1	MP TFAFAQEIAQQLMSLIINTFYSNKEIFLRELITNASDALDKIRYESLT	60
Query: 61	DPSKLDSGKELKIDITPNPQEERTLTVDTGIGMTKADLINNLGTLAKSGTKAFMEALQAG	120
Sbjct: 61	DPSKLDSGKELKIDITPNPQEERTLTVDTGIGMTKADLINNLGTLAKSGTKAFMEALQAG	120
Query: 121	ADISMIGQFGVGVFSAYLVAEKVVVITKHNDDQYAWESSAGGSFTVRADHGEPIGRGTK	180
Sbjct: 121	ADISMIGQFGVGVFSAYLVAEKVVVITKHNDDQYAWESSAGGSFTVRADHGEPIGRGTK	180
Query: 181	VILHLKEDQTEYLERVKEVVVKHQSFIGYPITLYLEKXXXXXVXXXXXVXXXXX 240	
Sbjct: 181	VILHLKEDQTEYLERVKEVVVKHQSFIGYPITLYLEKREKEISDDEEEKGKEERE	240
Query: 241	XXXXXXXXXXXXXXXXXXXXXXXJIDQEEELNKTKPIWTRNPDDITQSE	300
Sbjct: 241	XIDQEEELNKTKPIWTRNPDDITQSE	300
Query: 301	YGEFYKSLTNDWEDHLAVKHFSVEGQLEFRALLEIPRRAPFOLFENKKKKNNIKLYVRRV	360
Sbjct: 301	YGEFYKSLTNDWEDHLAVKHFSVEGQLEFRALLEIPRRAPFOLFENKKKKNNIKLYVRRV	360
Query: 361	FIMDSQELIPEYLNFIRGVYDLPNTISREMLOSKIKSVIRKNEVKKCLELFSELA	420

FIG. 15B

FINDSCDELIPYEYLNFIRG SEDLPLNISREMLQQSKILKVKRQIVKKCI SELA
 subjct: 361 FIMDSDELIPYEYLNFIRGVVDSEDLPLNISREMLQQSKILKVKRQIVKKCLUFSELA 420
 Query: 421 EDKENYKKPYEAPSKNLKLGIHEUDSTNRRLSELLRYHTSQSGDEMTSLSSEYVSRMKETQ 480
 EDKENYKKPYEAPSKNLKLGIHEUDSTNRRLSELLRYHTSQSGDEMTSLSSEYVSRMKETQ
 subjct: 421 EDKENYKKPYEAPSKNLKLGIHEUDSTNRRLSELLRYHTSQSGDEMTSLSSEYVSRMKETQ 480
 Query: 481 KSIYYITGESKEQVANSAPVERVRKRGPEVYMTEPIDEYCVQQLKEFDGKSLVSVTXXX 540
 KSIYYITGESKEQVANSAPVERVRKRGPEVYMTEPIDEYCVQQLKEFDGKSLVSVT
 subjct: 481 KSIYYITGESKEQVANSAPVERVRKRGPEVYMTEPIDEYCVQQLKEFDGKSLVSVTKED 540
 Query: 561 XXXXXXXXXXXXXXXXXKNLCKLMKEILDCKVEKVUTISNRLVSSPCCIVTSTYGTWA 600
 ; NLCKLMKEILDCKVEKVUTISNRLVSSPCCIVTSTYGTWA
 subjct: 561 LBLPEDBEEKKKMRSKAFENLCKLMKEILDCKVEKVUTISNRLVSSPCCIVTSTYGTWA 600
 Query: 601 NMERIMKAQALRDNSTMGYMAKKHLEINPDHPITVELRQKABADKNDKAVKDLVVLIFE 660
 NMERIMKAQALRDNSTMGYMAKKHLEINPDHPITVELRQKABADKNDKAVKDLVVLIFE
 subjct: 601 NMERIMKAQALRDNSTMGYMAKKHLEINPDHPITVELRQKABADKNDKAVKDLVVLIFE 660
 Query: 661 TALLSSOFSLEDPQTHSNRfYRMIKLGCGIXXXXXXXXXXXXXXIPPLEGDEDASRM 720
 TALLSSOFSLEDPQTHSNRfYRMIKLGCGI IPPLEGDEDASRM
 subjct: 661 TALLSSOFSLEDPQTHSNRfYRMIKLGCGIDEDEVTAEPSAVERDIPPLEGDEDASRM 720
 Query: 721 ERVD 724
 ERVD
 subjct: 721 ERVD 724
 CPU time: 0.15 user secs. 0.06 sys. secs 0.21 total secs.
 Lambda K H
 0.317 0.115 0.375
 Gapped
 Lambda K H
 0.257 0.0410 0.140
 Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 4890
 Number of Sequences: 0
 Number of extensions: 325
 Number of successful extensions: 1
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 0
 Number of HSP's gapped (non-prelim): 1
 length of query: 724
 length of database: 405,742,523
 effective HSP length: 134
 effective length of query: 590
 effective length of database: 405,742,389
 effective search space: 239388009510
 effective search space used: 239388009510
 T: 9
 A: 40
 X1: 16 (7.3 bits)
 X2: 129 (49.7 bits)
 X3: 129 (49.7 bits)
 S1: 41 (21.6 bits)
 S2: 78 (34.7 bits)

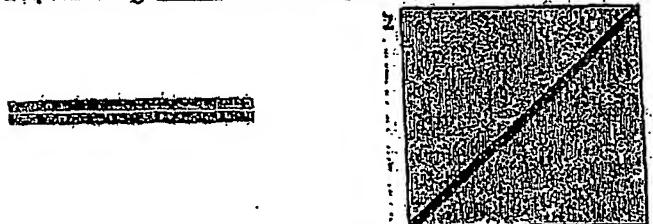
FIG. 16A

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4

Matrix SLOSUM62 gap open: 11 gap extension: 1
 x_dropoff: 50 expect: 10.00 wordsize: 3 Filter:

Sequence 1 gi_72220 heat shock protein 86 - mouse Length 733 (1 .. 733)

Sequence 2 gi_72223 heat shock protein 84 - mouse Length 724 (1 .. 724)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 1102 bits (2851), Expect = 0.0
 Identities = 561/733 (76%), Positives = 611/733 (82%), Gaps = 9/733 (1%)

Query: 1 MPEETQTQDQPMEEEEEVTFAPQAEIAQLMSLIIINTFYSNKEIPLRRELISNSDALDKIR 60
 Sbjct: 1 MPEEVHNG-----EEEVETFAFPQAFIAQLMSLIIINTFYSNKEIPLRRELISNSDALDKIR 55

Query: 61 YESLTDPSKLDSGKELWIVNUTPSKQDRLLTIVDTGIGMTKADLINNLGTIAKSGTKAFME 120
 Sbjct: 56 YESLTDPSKLDSGKELKIDLYIPNPQERTLTLVDTGIGMTKADLINNLGTIAKSGTKAFME 115

Query: 121 ALQAGADISMIGQFGVGFYSAYLVAEKVTVITKHNDDEQYAWESSAGGSFTVRIDTGEP 180
 Sbjct: 116 ALQAGADISMIGQFGVGFYSAYLVAEKVVVITKHNDDEQYAWESSAGGSFTVRADHGEPI 175

Query: 181 GRGTIVILHLKEDQTEYLEPERRIKETVKKHSQFIGYPITLFLVEKERXXXXXJXXXXXX 240
 Sbjct: 176 GRGTIVILHLKEDQTEYLBEPR+KE+VKKHSQFIGYPITL+EKER 235

Query: 241 XXOOXXXXLNKTKPIWTR 300
 Sbjct: 236 EKEEEDKEDEEKPKIEDVGSDDEDDSGKDKKKKTKKIKKIKYIDQEE---LNKTKPIWTR 291

Query: 301 NPDDITNEGYGEFYKSLTNDWEHLAVKHF\$VEGQLEPRALLF\$PRAAPFDLFENKKNN 360
 Sbjct: 292 NPDDITQESEYGEFYKSLTNWEDHLAVKHF\$VEGQLEPRALLF\$PRAAPFDLFENKKNN 351

Query: 361 NIKLYVRRVFIMDNCEELIPEYLNEIRGVVDSEDLPENISREMLQQSKILKVKIRKNLVKK 420

FIG. 16B

NIKLYVRRVFIMD+C+EL. [LNFIIRGVVDSEDLPLNISREMLQQSKILKVI +VKK
 Sbjct: 352 NIKLYVRRVFIMDSCDELIEYLNFIIRGVVDSEDLPLNISREMLQQSKILKVI.NIVKK 411
 Query: 421 CLELFTELAEDKENYKKFYEQPSKNIKLGIGHEDSQNRKYLSELLRY+TSASGDEMVSLSK 480
 CLELF+ELAEDKENYKKFYE PSRN+KLGIGHEDS NR+LSELLRY+TS SGDEM SL +
 Sbjct: 412 CLELPSELAEDKENYKKFYEAFSKNLKLGHEDSTNRRRLSELLRYHTSQSODEMTSLS 471
 Query: 481 YCTRMKENQKHIFYFITGETKDVANSAFVERLRKHCLEVIYMIPIDEYCVQQLKEFEGK 540
 Y +RMKE QK IY+ITGE+K+QVANSAPVER-RK G PV+YM 2PIDEYCVQQLKEP+GK
 Sbjct: 472 YVSRMKRKTQKSITYYTGESKEQVANSAFVERVRKRGFEVYXMTFIDEYCVQQLKEPDGK 531
 Query: 541 TLVSVTXXXXXXXXXXXXXXDOXXXXXXOONLCKIMKDILEKKVVKVVSNRLVTSPCCI 600
 +LVSVT NLCK+MK+IL+KKVEKV +SNRLV+SPCCI
 Sbjct: 512 SLVSVTKEGLELPEDEEKKMEEESAKFENLCKLMKEILDKKVVKTLISNRLVSSPCCI 591
 Query: 601 VTSTYGTANMERIMKAQALRDNSTMGYMAKKHLIENPDHSIIETLRQKAENDKNDKSV 660
 VTSTYGTANMERIMKAQALRDNSTMGYMAKKHLIENPDHSIIETLRQKAENDKNDKSV
 Sbjct: 592 VTSTYGTAMMERIMKAQALRDNSTMGYMAKKHLIENPDHPIVETLRQKAENDKNDKAV 651
 Query: 661 KDLVLLYETALLSSGFSLEDPQTHANRIYRMIKLGGLGIDEDDDPTVODTSAAVTEEMPL 720
 KDLV+LL+ETALLSSGFSLEDPQTH+NRUYRMIKLGGLGIDED+ T ++ SAAV +E+PPL
 Sbjct: 652 KDLVLLYETALLSSGFSLEDPQTHSNRIYRMIKLGGLGIDEDDEVTAEPAAVPDEIPPL 711
 Query: 721 EGDDDTSRM2EVD 733
 EGD+D SRM2EVD
 Sbjct: 712 EGDEDASRM2EVD 724

CPU time: 0.17 user secs. 0.01 sys. secs 0.18 total secs.

Lambda	K	H
0.316	0.134	0.372

Gapped		
Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DS: 5349
 Number of Sequences: 0
 Number of extensions: 384
 Number of successful extensions: 3
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 0
 Number of HSP's gapped (non-prelim): 1
 length of query: 733
 length of database: 405,742,523
 effective HSP length: 134
 effective length of query: 599
 effective length of database: 405,742,389
 effective search space: 243039691011
 effective search space used: 243039691011
 T: 9
 A: 40
 X1: 16 (7.3 bits)
 X2: 129 (49.7 bits)
 X3: 129 (49.7 bits)
 S1: 41 (21.6 bits)
 S2: 78 (34.7 bits)